

	AAT GGC TTA TTA TGC TGG AAC GTG AAA GGT CAT GTA GAT GTA GAA GAG	3024
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu	
	995 1000 1005	
5	CAA AAC AAC CAC CGT TCG GTC CTT GTT ATC CCA GAA TGG GAG GCA GAA	3072
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu	
	1010 1015 1020	
10	GTG TCA CAA GAG GTT CGT GTC TGT CCA GGT CGT GGC TAT ATC CTT CGT	3120
	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg	
	1025 1030 1035 1040	
15	GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT	3168
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His	
	1045 1050 1055	
20	GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA	3216
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu	
	1060 1065 1070	
25	GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG	3264
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly	
	1075 1080 1085	
30	ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT	3312
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr	
	1090 1095 1100	
35	GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA	3360
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser	
	1105 1110 1115 1120	
40	GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT	3408
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys	
	1125 1130 1135	
45	GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT	3456
	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr	
	1140 1145 1150	
50	GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT	3504
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile	
	1155 1160 1165	
55	GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA	3552
	Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu	
	1170 1175 1180	
60	CTC CTT ATG GAG GAA	3567
	Leu Leu Met Glu Glu	
	1185	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
1 5 10 15

Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn
20 25 30

Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn
35 40 45

Phe Val Pro Gly Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp
50 55 60

Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu
65 70 75 80

Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile
85 90 95

Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala
100 105 110

Phe Lys Glu Trp Glu Glu Asp Pro His Asn Pro Ala Thr Arg Thr Arg
115 120 125

Val Ile Asp Arg Phe Arg Ile Leu Asp Gly Leu Leu Glu Arg Asp Ile
130 135 140

Pro Ser Phe Arg Ile Ser Gly Phe Glu Val Pro Leu Leu Ser Val Tyr
145 150 155 160

Ala Gln Ala Ala Asn Leu His Leu Ala Ile Leu Arg Asp Ser Val Ile
165 170 175

Phe Gly Glu Arg Trp Gly Leu Thr Thr Ile Asn Val Asn Glu Asn Tyr
180 185 190

Asn Arg Leu Ile Arg His Ile Asp Glu Tyr Ala Asp His Cys Ala Asn
195 200 205

Thr Tyr Asn Arg Gly Leu Asn Asn Leu Pro Lys Ser Thr Tyr Gln Asp
210 215 220

Trp Ile Thr Tyr Asn Arg Leu Arg Arg Asp Leu Thr Leu Thr Val Leu
225 230 235 240

	Asp	Ile	Ala	Ala	Phe	Phe	Pro	Asn	Tyr	Asp	Asn	Arg	Arg	Tyr	Pro	Ile	
					245					250					255		
5	Gln	Pro	Val	Gly	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Ile	
				260					265					270			
	Asn	Phe	Asn	Pro	Gln	Leu	Gln	Ser	Val	Ala	Gln	Leu	Pro	Thr	Phe	Asn	
			275					280					285				
10	Val	Met	Glu	Ser	Ser	Ala	Ile	Arg	Asn	Pro	His	Leu	Phe	Asp	Ile	Leu	
		290					295					300					
	Asn	Asn	Leu	Thr	Ile	Phe	Thr	Asp	Trp	Phe	Ser	Val	Gly	Arg	Asn	Phe	
15	305				310					315					320		
	Tyr	Trp	Gly	Gly	His	Arg	Val	Ile	Ser	Ser	Leu	Ile	Gly	Gly	Gly	Asn	
					325					330					335		
20	Ile	Thr	Ser	Pro	Ile	Tyr	Gly	Arg	Glu	Ala	Asn	Gln	Glu	Pro	Pro	Arg	
				340					345					350			
	Ser	Phe	Thr	Phe	Asn	Gly	Pro	Val	Phe	Arg	Thr	Leu	Ser	Asn	Pro	Thr	
		355						360					365				
25	Leu	Arg	Leu	Leu	Gln	Gln	Pro	Trp	Pro	Ala	Pro	Pro	Phe	Asn	Leu	Arg	
		370					375					380					
	Gly	Val	Glu	Gly	Val	Glu	Phe	Ser	Thr	Pro	Thr	Asn	Ser	Phe	Thr	Tyr	
	385					390					395				400		
	Arg	Gly	Arg	Gly	Thr	Val	Asp	Ser	Leu	Thr	Glu	Leu	Pro	Pro	Glu	Asp	
					405					410					415		
35	Asn	Ser	Val	Pro	Pro	Arg	Glu	Gly	Tyr	Ser	His	Arg	Leu	Cys	His	Ala	
			420						425					430			
	Thr	Phe	Val	Gln	Arg	Ser	Gly	Thr	Pro	Phe	Leu	Thr	Thr	Gly	Val	Val	
		435						440					445				
40	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	Thr	Leu	Thr	Asn	Thr	Ile	Asp	Pro	
		450					455						460				
	Glu	Arg	Ile	Asn	Gln	Ile	Pro	Leu	Val	Lys	Gly	Phe	Arg	Val	Trp	Gly	
45	465					470					475				480		
	Gly	Thr	Ser	Val	Ile	Thr	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	
					485					490					495		
50	Arg	Arg	Asn	Thr	Phe	Gly	Asp	Phe	Val	Ser	Leu	Gln	Val	Asn	Ile	Asn	
				500					505					510			
	Ser	Pro	Ile	Thr	Gln	Arg	Tyr	Arg	Leu	Arg	Phe	Arg	Tyr	Ala	Ser	Ser	
		515						520					525				